

RT	domain-containing protein that interacts with BAI1. ";
RL	Biochem. Biophys. Res. Commun. 247:597-604 (1998).
CC	-1- FUNCTION: LIKELY TO BE A POTENT INHIBITOR OF ANGIOGENESIS IN BRAIN AND MAY PLAY A SIGNIFICANT ROLE AS A MEDIATOR OF THE P53 SIGNAL IN SUPPRESSION OF GLIOBLASTOMA. MAY FUNCTION IN CELL ADHESION AND SIGNAL TRANSDUCTION IN THE BRAIN.
FT	-1- SUBUNIT: INTERACTS WITH BAP1.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LIKELY TO BE CONCENTRATED AT CELL-CELL ADHESION SITES.
FT	-1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN BRAIN. REDUCED OR NO EXPRESSION IS OBSERVED IN SOME GLIOBLASTOMA CELL LINES AND CANCER TISSUES.
CC	-1- INDUCTION: BY P53.
CC	-1- DOMAIN: THE TSP1 REPEATS INHIBIT IN VIVO ANGIOGENESIS IN RAT CORNEA INDUCED BY BFGF.
CC	-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC	-1- SIMILARITY: CONTAINS 5 TSP TYPE-1 DOMAINS.
CC	-1- SIMILARITY: CONTAINS 1 GPS DOMAIN.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL: AB005297; BRA23647.1; -.
DR	Genew, HGNC:943; BAI1.
DR	MIM: 601682; -.
DR	InterPro: IPR000832; GPCR, secretin.
DR	InterPro: IPR000203; PKD_cys_rich.
DR	InterPro: IPR000834; TSP1.
DR	InterPro: IPR000879; hormn_receptor.
PFAM: PF00002; 7tm_2; 1.	
DR	Pram; PF00090; tsp_1; 5.
DR	Pram; PF01825; GPS_1.
DR	Pfam; PF02793; HRM_1.
DR	SMART; SM000303; HormR_1.
DR	SMART; SM00008; HormR_1.
DR	SMART; SM00209; TSP1_5.
DR	PROSITE; PS50221; GPS_1.
DR	PROSITE; PS00649; G_Protein_Recep_F2_1; FALSE_NEG.
DR	PROSITE; PS00650; G_Protein_Recep_F2_2; FALSE_NEG.
DR	PROSITE; PS50227; G_Protein_Recep_F2_3; 1.
DR	PROSITE; PS50261; G_Protein_Recep_F2_4; 1.
DR	PROSITE; PS50092; TSP1_5.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Repeat; Cell adhesion.
FT	SIGNAL 1 30 POTENTIAL.
FT	CHAIN 31 1584 BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1.
FT	DOMAIN 31 948 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 949 969 1 (POTENTIAL).
FT	DOMAIN 970 980 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 981 1001 2 (POTENTIAL).
FT	DOMAIN 1002 1008 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 1009 1029 3 (POTENTIAL).
FT	DOMAIN 1030 1052 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 1053 1073 4 (POTENTIAL).
FT	DOMAIN 1074 1093 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 1188 1584 5 (POTENTIAL).
FT	DOMAIN 261 316 TSP TYPE-1.
FT	DOMAIN 354 408 TSP TYPE-1.
FT	TRANSMEM 1115 1136 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 1137 1157 6 (POTENTIAL).
FT	DOMAIN 1158 1166 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 1167 1187 7 (POTENTIAL).
FT	DOMAIN 1188 1584 CYTOPLASMIC (POTENTIAL).
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FT	DOMAIN	1425	1430	POLY-PRO.	RL	DNA Res. 3:137-155(1996); Integral membrane protein (Potential).
FT	SITE	231	233	CELL ATTACHMENT SITE (POTENTIAL).	CC	-1- SUBCELLULAR LOCATION: BELONGS TO THE UPF0003 FAMILY.
FT	DOMAIN	1365	1584	NECESSARY FOR INTERACTION WITH BAP1.	CC	-1- SIMILARITY: Ref.2 sequence differs from that shown due to a
FT	DOMAIN	1581	1584	INDISPENSABLE FOR INTERACTION WITH BAP1.	CC	-1- CAUTION: Ref.2 sequence differs from that shown due to a
FT	CARBOHYD	64	64	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	framshift in position 77.
FT	CARBOHYD	401	401	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	
FT	CARBOHYD	607	607	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	CARBOHYD	692	692	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
FT	CARBOHYD	844	844	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	the European Bioinformatics Institute. There are no restrictions on its
FT	CARBOHYD	877	877	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	use by non-profit institutions as long as its content is in no way
FT	CARBOHYD	881	881	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	modified and this statement is not removed. Usage by and for commercial
SQ	SEQUENCE	1584	AA:	173531 MW: DEA8F78C77874513 CRC64;	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Query Match		4.6%	Score 105.5; DB 1; Length 1584;	CC		
Best Local Similarity		23.0%	Pred. No. 4.5; Pred. No. 4.5;	CC		
Matches	65;	Conservative	38; Mismatches 98; Indels 81; Gaps 12;	CC		
Qy	193	ISABEPLGRGVLMFSLVSVTYGATLNMMLAIQKYDDYKIRGLPLEVLCITIWRLB--	250	DR	EMBL; DR00183; AAC73895.1; ALT_INIT.	
Db	935	LSADANMEKATLPGSTVTLI-VGGGVSSTLMLVITY-----VSWRYIRSE 979		DR	EMBL; DR0717; BAA5474.1; _	
Qy	251.	--ITSRLILV-----LFSATIKLKAVPFLVNLFLIFEFWV 286		DR	EMBL; DR0718; BAA5479.1; ALT_FRAME.	
Db	980	RSVTLINFCLSIISNALILIGOTQTRNKMVTAAFLHF---FFLSSFCMVLTTEAMQ 1035		DR	EMBL; DR0718; BAA5480.1; ALT_FRAME.	
Qy	287	KFVRSGAOPNN-T-EKNSPVRG---TFLVLSITVL---YAGINFSGSWALQQLRADR 337		DR	EcoGene; EG13320; yBio.	
Db	1036	SYMAVTGHLRNLRLRFLCLGNGLPALVAISVGFTAKGYSITNNY CWLSL--	1087	DR	InterPro; IPR001810; MSion_channel.	
Qy	338	DLYDGKONWGHMGHYSYRLVENVYTMVLFKEFKGVK-----VLLNYC--HS 381		DR	Pfam; PF00924; MS_channel.1;	
Db	1088	--EGGLIAYFVPEAAVVLNNNVTGILVNLKLSKDGITDKKKLKERAGASLMSCVVLP 1144		DR	PROSITE; PS01246; _UPF0003; FALSE_NEG.	
Qy	382	LIALQLIAYLISIDFMLLFFQYIPLSLTSFLTNVVDYLHCV 423		DR	KW_Hypothetical protein; Transmembrane; Complete proteome.	
Db	1145	LLALTTWNSAVLAVYDRRSALFQTLFAVFDSLEGIVMVHCl 1186		DR	TRANSMEM 9 29	
RESULT 5				FT	TRANSMEM 143 163	
YBIO_ECOLI	STANDARD; PRT; 741 AA.			FT	TRANSMEM 143 163	
ID	YBIO_ECOLI			FT	TRANSMEM 225 205	
AC	P75783; Q9R7S0; Q9R7S2; Q9RBG5;			FT	TRANSMEM 268 288	
DT	15-JUL-1998 (Rel. 3.6, Created)			FT	TRANSMEM 294 314	
DT	15-DEC-1998 (Rel. 3.7, Last sequence update)			FT	TRANSMEM 343 363	
DT	15-JUN-2002 (Rel. 4.1, Last annotation update)			FT	TRANSMEM 374 394	
DE	Hypothetical protein yBio.			FT	TRANSMEM 432 452	
GN	YBIO OR B0804.			FT	TRANSMEM 466 486	
OS	Bacteriorrhizal membrane protein.			FT	TRANSMEM 509 529	
OC	Proteobacteria; Gamma subdivision; Enterobacteriaceae;			FT	TRANSMEM 533 553	
OC	Escherichia coli.			FT	TRANSMEM 562 582	
NCBI_TaxID	562.			FT	TRANSMEM 608 628	
RN	SEQUENCE FROM N.A.			FT	TRANSMEM 662 682	
RC	STRAIN=K12 / MG1655;			FT	DOMAIN 25 30	
RX	MEDLINE:97426617; PubMed=9278503;			FT	POLY-LEU.	
RA	Blattner R.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			FT	SEQUENCE 1903 MW: 69B0A27678976DB5 CRC64;	
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			FT	SEQUENCE 741 AA: 81903 MW: 69B0A27678976DB5 CRC64;	
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			FT	Query Match 4.5%; Score 104.5%; DB 1; Length 741;	
RA	Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12.";			FT	Best Local Similarity 19.5%; Pred. No. 2.3;	
RT	Science 27:1453-1474(1997).			FT	Matches 96; Conservative 91; Mismatches 173; Indels 133; Gaps 25;	
RL				FT	YMDRYVEIPBEPNVPVSSLEEDVIRGANPRTPPFSIESTFL-----YCEAAASAL 52	
RN	SEQUENCE FROM N.A.			Db	66 IDQLRVTAATPAPPEPV-----PKIVPPTLVEEQTVLQKVTEVSRHGEALSAR 113	
RC				Qy	53 YMVRIYRK-----NSETYRMTY-----FSEFFMFESSIMVQLTLYFHRDLA- 93	
RX	MEDLINE:97061202; PubMed=890232;			Db	114 F-COLYRNTGSPHKPNPQTCFSNALTHFSMLAVLVFGRYW---LIRLCALPLYRKGQ 168	
RA	Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,			Qy	94 ---KDPPLSLFNLH---ILGPVYIRCLEAMIKYTLWKEQEPPYVSILRKMLIDGE 147	
RA	Ikeno T., Inada T., Itoh T., Kajihara M., Kansai K., Kashimoto K.,			Db	169 WAKQNRNRSVNLQPLAMIGAT-----DILLLAQLTLPVQ 206	
RA	Kitamura S., Makino K., Masuda S., Nishimoto H., Nishio Y., Saito N.,			Qy	148 VLIIEWVGHSLIRTLAMHRYAKRMSQTQAFGLSVPLQTY-----QLYVSLISAEPV--LG 200	
RA	Sanpei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,			Db	207 -VLSDNLNAGSRTIAFOQLFLNAFALIEFKAVRLIFCPNVAYELRPTIQDESARYMS 265	
RT	"A 718-kb DNA sequence of the Escherichia coli K-12 genome			Qy	201 RVVLMVFSLSVYTYGATLCMLAIQKYDDYKTRLGPL-----VLCITIW-----RTL 249	
RT	corresponding to the 12.7-28.0 min region on the linkage map."			Db	266 RRSWLSLIG-YGL---LIVLFSATLK-----LKVPLVNLFLILFEPWIKFNRSGAQM 219	
RA	Yano M., Horiuchi T.,			Qy	250 EITSRLL---LIVLFSATLK-----LKVPLVNLFLILFEPWIKFNRSGAQM 296	
RA	Yano M., Horii T., Tagami H., Takemoto K., Wada C., Yamamoto Y.,			Db	320 EITQHLLNFAEHLAFLFPLAFAYWWHLASAYFQLRIADR-----D-LVVKGQNWHGM 367	
RT				Qy	297 NNIKNEFNSRVLGTLVVLISVTLIYAGINFSWSAQLRIADR-----D-LVVKGQNWHGM 350	
RA	NSLKFMDGATRSLAIIGIAFVSGM-FSRWLAKTITLSPHTORNYPFLQKRLNGWLSA 426			Db	368 NSLKFMDGATRSLAIIGIAFVSGM-FSRWLAKTITLSPHTORNYPFLQKRLNGWLSA 426	

Qy	351	LHYSVRLVENAVMVLVKEFVYKVLNLYCHSLSIALQIJAYLISIDFMLLFFOYL--HPL	408	QHPRTVENSEPPFTEA 444
Db	427	LKTARILTVCAVMILLISAWGLFDFNWLQN-GAGQKTVTDLIRI-ALIIFSSAVGWTFL	484	QHHPN--DSNSPSDDES 360
Qy	409	RSLFTHNVVDYLH 421		
Db	485	ASLIEENRLASDIH 497		
RESULT 6				
YMP0 YEAST				
ID YMP0 YEAST				
PRT; 405 AA.				
STANDARD;				
AC Q03657;				
DT 01-NOV-1997 (Rel. 35, Created)				
DT 01-NOV-1997 (Rel. 35, Last sequence update)				
DT 01-NOV-1997 (Rel. 35, Last annotation update)				
DE Hypothetical 46.9 kDa protein in PLB1-HX2 intergenic region.				
DE YN010W OR YM8270.13.				
OS Saccharomyces cerevisiae (Baker's yeast).				
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.				
OX NCBI_TaxID:4932;				
[1]				
RN SEQUENCE FROM N.A.				
RP STRAIN=S238C / AB972;				
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;				
RA submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.				
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC modified and this statement is not removed. Usage by and for commercial				
CC entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).				
EMBL; 248613; CAA8826.1; -.				
DR SGD; S0004612; YMR030W.				
KW Hypothetical protein; Transmembrane.				
TRANSMEM 52 72	POTENTIAL.			
FT TRANSMEM 77 97	POTENTIAL.			
FT TRANSMEM 104 124	POTENTIAL.			
FT TRANSMEM 179 199	POTENTIAL.			
FT TRANSMEM 224 244	POTENTIAL.			
FT TRANSMEM 255 275	POTENTIAL.			
FT TRANSMEM 300 320	POTENTIAL.			
SEQUENCE 405 AA; 46872 MW; AF019859073E134E CRC64;				
Query Match 4.4%; Score 102.5; DB 1; Length 521;				
Best Local Similarity 22.0%; Pred. No. 1.6;				
Matches 70; Conservative 54; Mismatches 95; Indels 99; Gaps 18;				
Matches 72; Conservative 70; Mismatches 139; Indels 95; Gaps 16;				
Qy 178 LGSYPPOLTYVLSISAEVPLGR--VVLAVPSLIVSVTYGATLCLNMLAIQIKY--DDYKI 233				
Db 91 IASIRIISYIYL-ITPEYITLRLQSMVPIQLI--LLRTLSKRYPDEKY 137				
Qy 234 R-LGPLEV-----CITIWRTL-EITISPLLILVLFATSLKLKAVPFLYLNFL 278				
Db 138 QNLTDVESSLHLIRHWFPEFSCINRPKFLSDDWNKLQIKSLSTFLNLIKPSKIKLAFYK 197				
Qy 279 II-LFEPWIKFWRSQAGMPNNIEKNSRVTGFLVVLISVTLYAGINFSCMSALQLIADR 337				
Db 198 ILKEFDP--NFKRCAFQWDDDNWFLALFATVQLVTFINSLNWLNSLAQGL-- 252				
Qy 338 DLVDKGQNWGMGL--HYSVRLVENIVMVLV--FKEFGV 372				
Db 253 ---GSIIGSLGLLIVESLPLPQAILYKLSQGFLKLLVSLQGDTLKITYLIFGA 307				
Qy 373 KVLLNLYCHSLSIALQIJAYLISIDFMLLFFOYL--LRFQYLH-LRSLETHNVVDLHCVCC 426				
Db 308 K-----NISALPWFALQFOMSLDPIYIGGOTIYIYYPCLR-----H 344				
Qy 331 Q---LRLA-----DRDLYDKGQNWGMGLHYSVRLVENIVMVLVF---KFGV 372				
Db 372 EGPTGKYLASCFCMFDIPDRVLYLTLGM-----YFAUSLCLLNLTTFSKSSKSFNL 428				

Qy	373 KVLLN-----YCHSLIALQLLIAYLISIDFIMLFFOYLHPLRSLETFHNVVDYLHCVY 424	Qy	188 LYVSL--ISAEVPLGRVWLMVFSLVSTVYG-----ATLCNMLAIOQKYDD 230
Db	429 KIRNNEQEYKNSSAVSLISVFQVAMTAYVASSLIVYRRDPHEYFHII-----LC 483	Db	37 LHISTNIGYLTMGAFFLILINLSTNYKLIGNWSISEQESLYATLHSIVVNQINPKN 96
Qy	425 CHQHPRTRYENSEPPF 440	Qy	231 YKIRLGPLEYLCITIWRTELEITSLRLLVLFATKLKAVPFLVLFNLLFLFEPWTKFWR 290
Db	484 IYVSLKLQLHLTCPEF 499	Db	97 GQIYFPFIYALFIFI-----LNNLGMVYSSFASTSHFLVLTFLSFTIVLGAFLGQK 151
RESULT 8			
ATP6 PODAN	ATP6 PODAN	STANDARD;	PRT;
ID	AC	P15594;	Rel. 14. Created)
DT	DT	01-APR-1990	(Rel. 14, Last sequence update)
DT	DT	15-JUN-2002	(Rel. 41, Last annotation update)
DE	DE	ATP synthase A chain	(EC 3.6.3.14) (Protein 6).
GN	GN		
OS	OS	Podospora anserina.	
OG	OG	Mitochondrion.	
OC	OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
OC	OC	Sordariidae; Lasiobasidiaceae; Podospora.	
OX	OX	NCBI TaxID=5145;	
RN	RN		
RP	RP	SEQUENCE FROM N.A.	
RC	RC	STRAIN=S and A;	
RX	RX	MEDLINE=9125610; PubMed=2975708;	
RA	RA	Cummings D.J.; Domenico J.M.;	
RT	RT	"Sequence analysis of mitochondrial DNA from Podospora anserina. Pervasiveness of a class I intron in three separate genes.";	
RL	RL	J. Mol. Biol. 204:815-839 (1988).	
RN	RN	[1]	RN [2]
RP	RP	COMPLETE GENOME.	
RC	RC	STRAIN=S	
RA	RA	MEDLINE=00291512; PubMed=2357736;	
RT	RT	Cummings D.J.; McNally K.L.; Domenico J.M.; Matsusura E.T.; Domenico J.M.; Matsusura E.T.; Sordariidae; Podospora anserina";	
RT	RT	"The complete DNA sequence of the mitochondrial genome of the anserina";	
RL	RL	Curr. Genet. 17:375-402 (1990).	
CC	CC	-I - FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.	
CC	CC	-I - CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).	
CC	CC	-I - SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA (3), BETA (3), GAMMA (1), DELTA (1), EPSILON (1). CF (0) HAS THREE MAIN SUBUNITS: A, B AND C.	
CC	CC	-I - SUBCELLULAR LOCATION: Integral membrane protein.	
CC	CC	-I - SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.	
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	CC	DR EMBL: X50026; CAA38770_1; -	
CC	CC	DR EMBL: X13602; CAA3825_1;	
DR	DR	InterPro: IPR000568; ATPSynth_Asub.	
DR	DR	PFam: PF00119; ATP_Synth_A; 1.	
DR	DR	PRINTS: IPR00123; ATPase_A.	
DR	DR	TIGRFAMs: TIGR01131; ATP_Synth_6_or_A; 1.	
DR	DR	PROSITE: PS00449; ATPase_A; 1.	
KW	KW	Hydrogen ion transport; CF (0); Mitochondrion; Transmembrane.	
SQ	SQ	SEQUENCE 264 AA; 29317 MW; 8029AAE8402A17 CRC64;	
DR	DR	Query Match 4.3%; Score 100.5; DB 1; Length 459;	
DR	DR	Best Local Similarity 18.9%; Pred. No. 2.6; Mismatches 75; Mismatches 79; Conservative Matches 79; Indels 133; Gaps 20;	
Qy	67 MTYT-----PSFPMSSIMVQLTLLFVHRLAKDKPLS--LFLMHLIGG--PVIRCLEA 116	Qy	67 MTYT-----PSFPMSSIMVQLTLLFVHRLAKDKPLS--LFLMHLIGG--PVIRCLEA 116
Db	108 MTFPATLFFYILEATLIP-TLIIITWGNQYERLNAGFYFLPYTLTSPLL-----161	Db	108 MTFPATLFFYILEATLIP-TLIIITWGNQYERLNAGFYFLPYTLTSPLL-----161
Qy	117 MIKVLTWKEEQQEPYPSLTRKOMLIDGEVILWEVGHSGIRTL-AMHRNAYKERMQIO 175	Qy	117 MIKVLTWKEEQQEPYPSLTRKOMLIDGEVILWEVGHSGIRTL-AMHRNAYKERMQIO 175
Db	162 -----IATHIQNLTGSGANLL--IQSTOTUPSSWSNAFLWACMM 201	Db	162 -----IATHIQNLTGSGANLL--IQSTOTUPSSWSNAFLWACMM 201
Qy	176 AFLGSVPQLTYQLVYSLISEEVPL-GRVVLMSLVSVTYGATLCNMLAIOQKYDDYKIR 234	Qy	176 AFLGSVPQLTYQLVYSLISEEVPL-GRVVLMSLVSVTYGATLCNMLAIOQKYDDYKIR 234

Db	202	AFMVKMPFLYGLHLWLPKAHVEAPIAGSKVLAAILKLGGYMLRITMI	249	Matches 64; Conservative 22; Mismatches 68; Indels 116; Gaps 13;
Qy	235	LGPL-----EVLCITIWRTEBITSRLILVLFSATLKLKAVPFLVNFLLIE-PWIK	287	Qy 205 MYSLSVSYGATLCNMIAIQKYYDKYKIRGPLE---VLCITIWRTEBITSRLILVL 260
Db	250	LNPLTSYMAYPPLMLSLWGMINTMSICLRODLSKLIAYSSYHMLAVAVLQOTW-S	308	Db 1 MFSLAAVEVGTHL-----YWEIGGLEEVHGCVLLT-WLVIAAIIITLAIL- 44
Qy	288	PWRSQAM-----PNIEKNSR-----VGTLLVLISVTLLYAGTINFSC	326	Qy 261 FSTTLKLKAVPFLVNFLLIE-----PWIKP-----WRSG 292
Db	309	YMGATALMIARGLTSSVLFCLANSYERTSRTMILARGLQTLPLMAMWNLASLT--	365	Db 45 ---GTLKLEQPKVPSQYVNFESYVSGIAKDOGEHYRPWVPPVGTLFLFIFVANW-LG 101
Qy	327	WSALQRLADRLDVLQDGQNWHGMGLHYSVRLVENTVNL-VFKFPGYKVLNYCHSIIAL	385	Qy 293 AOMP-----NINTEKNFSRVTGLVLLSIVTLLYGINFSCWMSALQLRADR 337
Db	366	-----NLAPPFLNLVGEFLVMSSEFSWNNTII-----LMGT	398	Db 102 ALPWKLHLPEGEGLAAPTNIDNTVA---LSLLTSISYFAGFK----- 143
Qy	386	QLIIAYLISIISDFMLLFFQYLHPLRSLFTHNVYDYLHCVCCQHOPRTVENVSEPPFETE	443	Qy 338 DLVDKGQNWHGMGLHYSVRLVE-----NVI-----MVLYKEKFFG-----VVKL 375
Db	399	NIITAYLSL-YMLITQ-----RGKYZTH-----INNIKPSFRE	433	Db 144 -----EKLGFYFARYISPTPIFLPINILDEFTKPLSLSFRFLGNILADEIVVSVL 193
RESULT 10				
ATPI_OCHNE		STANDARD;	PRT;	233 AA.
AC	Q40607;			RESULT 11
DT	01-NOV-1997	(Rel. 35, Created)		ACHO_HUMAN STANDARD;
DT	15-JUN-2002	(Rel. 41, Last annotation update)		PRT; 458 AA.
DE		ATP synthase A chain precursor (EC 3.6.3.14) (Subunit IV).		AC Q05901; Q15827;
GN		ATPI.		DT 01-JUN-1994 (Rel. 29, Created)
OS		Ochrophaea neapolitana.		DT 01-NOV-1997 (Rel. 35, Last annotation update)
OG		Chloroplast.		DT 15-JUN-2002 (Rel. 41, Last annotation update)
OC		Eukaryota; Haptophyceae; Isochrysidales; Ochrophaera.		DB Neuronal acetylcholine receptor protein, beta-3 chain precursor.
OX		NCBI_TaxID:5137;		GN Homo sapiens (Human)
RN		[1]		OS Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RP		STRAIN=CMP 593;		OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RC				NCBTI_TaxID:9606;
RN				RN [1]
CC				RP SEQUENCE FROM N.A.
CC				RC TISSUE=Substantia nigra;
CC				RX MEDLINE=97062879; PubMed=8906617;
CC				CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL. IT MAY PLAY A
CC				CC -1- DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.
CC				CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + Phosphate +
CC				CC H(+) (Out).
CC				CC "SUBUNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CP(1) - THE CATALYTIC
CC				CC - CORE - AND CP(0) - THE MEMBRANE PROTON CHANNEL. CP(1) HAS FIVE
CC				CC SUBUNITS: ALPHA (3), BETA (3), GAMMA (1), DELTA (1), EPSILON (1). CP(0)
CC				CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC				CC SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
CC				CC - thylakoid membrane.
CC				CC - SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
CC				CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC				CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC				CC use by non-profit institutions as long as its content is in no way
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CC				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC				CC
DR				DR EMBL: EMB67535; 1.
DR				DR InterPro: IPR000568; ATPsynth_Asub.
DR				DR Pfam: PF00119; ATP-synth_A.
DR				DR TIGRFAMs: TIGR01131; ATP synth_6_or_A_1.
DR				DR PROSITE: PS00449; ATPase_A_1.
KW				KW Hydrogen ion transport; CP(0); Chloroplast; Transmembrane; Signal.
FT				FT SIGNAL 1 ? BY SIMILARITY.
FT				FT CHAIN 2 ? BY SIMILARITY.
FT				FT TRANSMEM 27 47 POTENTIAL.
FT				FT TRANSMEM 84 104 POTENTIAL.
FT				FT TRANSMEM 192 212 POTENTIAL.
SQ				SEQUENCE 233 AA; 25721 MW; 6EEA74DE0887D6F1 CRC64;
CC				CC Score 99; DB 1; Length 233;
CC				CC Best Local Similarity 23.7%; Pred. No. 1.6;

MEMBRANE.

- I - SUBUNIT: NEURONAL AChR SEEKS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND BETA.
- I - SUBCELLULAR LOCATION: Integral membrane protein.
- I - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DR Putative gustatory receptor 64a.
 DE GR64A OR CG14986.
 DS Drosophila melanogaster (Fruit fly)
 DC Eukaryota; Metazoa; Arthropoda; Mandibulata;
 DC Insecta; Pterygota; Neoptera; Endopterygota;
 DC Muscomorpha; Ephydriodea; Drosophilidae; Drosophila
 DX NCBI_TAXID=7277;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN_BERKELEY ; PubMed=10731132;
 RP MEDLINE=20196006 ; PubMed=10731132;
 RP 2X

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CC DR EMBL; AE003480; AAF47824.1; ALT_SEQ.
 DR FlyBase; FBgn0045479; Gr64a.
 KW Hypothetical protein; Receptor; G-protein coupled receptor;
 DOMAIN 1 Transmembrane; Glycoprotein; Multigene family.
 PT DOMAIN 1 61 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 62 82 1 (POTENTIAL).
 PT DOMAIN 83 95 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 96 116 2 (POTENTIAL).
 PT DOMAIN 117 128 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 129 149 3 (POTENTIAL).
 PT DOMAIN 150 185 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 186 206 4 (POTENTIAL).
 PT DOMAIN 207 238 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 239 259 5 (POTENTIAL).
 PT DOMAIN 260 321 CYTOPLASMIC (POTENTIAL).
 PT TRANSMEM 322 342 6 (POTENTIAL).
 PT DOMAIN 343 351 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 352 372 7 (POTENTIAL).
 PT DOMAIN 373 456 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .). (POTENTIAL).
 FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .). (POTENTIAL).
 SQ SEQUENCE 456 AA; 52822 MW; 5466974C73495D6C CRC64; -----

Query Match Score 98.5; DB 1; Length 456;
 Best Local Similarity 20.7%; Pred. No. 3.6%; Mismatches 60; Indels 111; Gaps 21;

Qy 8 PEEPPNVDPV--SSLEEDVIRGAN-PRFT-----PPFSILFSTFLYCGRAASALYMV 55
 Db 27 PETPPPKFEDPSNLNPLASEKLPNVTNLDFRAVFP-----PMPLAQCVATMPL 79
 Qy 56 RIYRKNSETYRTM-TESFPMFSSIMVQTLIFVFRDLAKDKPLSLFMAHLTLIGPVIR-- 112
 Db 80 GIRESNPRVRREPAYKSIPMFVLTIFMIASTSILE-----LSMFTHLKIGITAKNF 129
 Qy 113 -----CLEARMIKYTL-----WKKEE-----QEEPYSLTRKMLIDGEEVILIEWEVSIRL 147
 Db 130 VGLVFFGCVLSAYVFLAKKWPAYVRIWTRTEIPFTKPPYEIKPNLSSRVQL--AA 186
 Qy 148 VLIIEWVGHSTRTLAMER---NAYKRNQSIQAFQFLGSVP-----QTYQIVLVSLSAEV 197
 Db 187 LAI---IGLSGEHALYQVSALISYTRIQMCANITYPSFNIMQNYDVFQQL--- 239
 Qy 198 PLGRVYLMVFSLVSVTYGATLGNML-----AIIQKYYDDYKIRLGPL--EVLK 242
 Db 240 PYSPPIAVLILIN---GA---CTFWNNTYMDLFIMIISKGLSYRFQITTRIRKLEHBEVC 294
 Qy 243 ITIW-----RTLE-ITSRLLIVLFSATLKLAKVPLVLNLILEP--WIKF 288
 Db 295 ESVFIQTREHYWKMCELLFVDSAMSSHILLSCVNLYNLFVCTQLNVFNKLWRPINVIYF 354
 Qy 289 WRS 291
 Db 355 WTS 357

RESULT 13
 ID TC10_YEAST STANDARD; PRT; 684 AA.
 AC PS0273;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DB TCM10_protein
 GN TCM10 OR YPBP350C OR D9476.9
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryotes; Fungi; Ascomycota; Saccharomyces; Saccharomyces
 OC Saccharomyces cerevisiae; Saccharomyces; Saccharomyces
 OC Saccharomyces; Saccharomyces; Saccharomyces
 OC Saccharomyces; Saccharomyces; Saccharomyces
 OC Saccharomyces; Saccharomyces; Saccharomyces
 NCBI_Taxid=4932;

RN [1] SEQUENCE FROM N.A.
 RP STRAIN=GH125;
 RC Zhang Y, Robinson K.M., Lenire B.D.;
 RA submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [2] SEQUENCE FROM N.A.
 RP Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favell A., Fulton L., Gattung S., Greco T., Kirten J., Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rieken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox D., Wohlbom P., Vaudin M., Wilson R.;
 RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; U32306; AAA74031.1;
 DR EMBL; U28372; AAB64786.1;-----
 DR SGD; S0002758; TCM10;
 DR CONFLICT 592 684 GARSWNKILPFGGEIRHMALIQIKDQGPPEPKNFDETLLI
 FT TELVNETNKEPTDNEFEDGKFRNDDVNKCT
 FT NIRETLLKSLN -> EHAPDTMRYSVGALKSGIWL (IN
 FT REF 2)
 SQ SEQUENCE 684 AA; 79755 MW; A88928484F8E49A4 CRC64;
 Qy Query Match Score 98.5; DB 1; Length 684;
 DB Best Local Similarity 18.7%; Pred. No. 5.7%;
 DB Matches 90; Conservative 60; Mismatches 163; Indels 169; Gaps 19;
 Qy 31 FPPPSILFSTFLYCGEASALYMVRIYRNSETYRMTYTFSSFM-----75
 DB 173 FLKSDVLLFMSNYCTRFTNRLI-----KGTEMERQLAFTQFLDENTIKFIMEVKLK 226
 Qy 76 -----FSSIMYQTLT-----IFVHRDLAKDKPL-----SLF 101
 DB 227 LHFTDSLIALVNLVKAKNFRFPIKVFQIOALLQKLEHQYSGDKOAKQKNLYVKFNNTLL 286
 Qy 102 MHLILGPVIRCLEAMIKYTLWIKKEOEPYSLTRKMLIDGEEVILIEWEVSIRL 161
 DB 287 YYLLKSGNV-----ELF1KTF-----QEEBLFVSSGLLNHIDQNEHILNPFIHYLNLL 336
 Qy 162 AMERNAVYKRMQSQIQAFLGSVPOLTYQVLSLISAEVPLGRVLMVFSVTVGATLCNM 221
 DB 337 RI-SNRQEEFLNVISLOSSPLMKYKLKFELNGE-----LIASFAFRDPKLVCKY 387
 Qy 222 LAIQKYYDKYKIRGLPLEVLCITIWRTL-BITSRLLILVLFSATLKLAKVPLVLFNLFL 280
 DB 388 L-----LSYSSKASANTLNALGIWGMLYHSKSTTLTAPLARELNK-----430
 Qy 281 LFPPIKWEWRSGQMPNNEKNSRVTGLVVLISVTIYAGINFSCHMSLQLRAADRDLV 340
 DB 431 -----NNLPTNMRIGSPVPLTELYRSLSS--SSVSL-----464
 Qy 341 DKQGNWGHMGHLYSVRLVENVIMLVFKFFG-----VKVLLNYCHSL 382
 DB 445 ESSQ-----PKNCLDLYKTKYKSFSEBAHKYRYMRNDTGILNVFLNIR 510
 Qy 383 IALQLIAYLISIDFMLLFFQYLHPL-----RSLETHNVNDYLHCVCCHOHPRTREVN 435
 DB 511 QAREPRLAYNVLDF-----ISQPFARKVVLTTLCPSFIRV-----KHNHTLQAEI 558
 Qy 436 SE 437
 DB 559 SE 560

RESULT 14	TRANSMEM	965	985	POTENTIAL.
YD56_SCHPO STANDARD	TRANSMEM	992	1012	PHOSPHORYLATION (BY SIMILARITY).
ID YD56_SCHPO	MOD. RES	408	408	MAGNESIUM (BY SIMILARITY).
Q10309;	FT METAL	770	770	MAGNESIUM (BY SIMILARITY).
AC 01-OCT-1996 (Rel. 34, Created)	FT METAL	774	774	MAGNESIUM (BY SIMILARITY).
DT 01-OCT-1996 (Rel. 34, Last sequence update)	SEQUENCE	1033	AA:	D57C467427D0C6D6 CRC64;
DT 15-JUN-2002 (Rel. 41, Last annotation update)	Query Match	4	3 %;	Score 98.5 ; Pred. No. 9 ;
DE Potential phospholipid-transporting Atase C6C3_06C (EC 3.6.3.1).	Best Local Similarity	19.8 %	;	Gaps 15 ;
GN SPAC6C3_06C.	Matches 62 ; Conservative	55	;	Mismatches 91 ; Indels 105 ; Gaps 15 ;
OS Schizosaccharomyces pombe (Fission yeast).	Qy 46 GEAS--A ₁ Y ₂ M ₃ Y ₄ R ₅ K ₆ N ₇ S ₈ E ₉ ;	;	;	;
OC Schizosaccharomyces; Fungi; Ascomycota; Schizosaccharomyces;	Db 792 GQ03LADDSVKEFHSYVSRLLWHGRISYKQTSKLMVTHRGULISYCVQVYVVISAF	;	;	;
OC Schizosaccharomycesales; Schizosaccharomycesaceae;	;	;	;	;
OX NCBI TaxID=4996;	;	;	;	;
RN [1]	;	;	;	;
RP SEQUENCE FROM N.A.	;	;	;	;
RC STRAIN=972;	;	;	;	;
RX MEDLINE=21848401; PubMed=11659360;	;	;	;	;
RA Seguros J.V., Peat N., Hayles J., Baker S., Basham D., Bowman S.,	;	;	;	;
RA Brooks K., Brown D., Brown R., Chillingworth T., Churcher C.M.,	;	;	;	;
RA Collins M., Connor R., Cronin A., Davis P., Fraser A.,	;	;	;	;
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,	;	;	;	;
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,	;	;	;	;
RA James K., Jones L., Leather S., McDonald S., McLean J.,	;	;	;	;
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,	;	;	;	;
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,	;	;	;	;
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,	;	;	;	;
RA Skelton J., Simmonds M., Squares R., Stevens K.,	;	;	;	;
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,	;	;	;	;
RA Weltjens I., Vansreels E., Vansreels E., Röben J., Rymond B.,	;	;	;	;
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,	;	;	;	;
RA Borzym K., Zimmermann W., Weller H., Wambutt R., Pohl T.M.,	;	;	;	;
RA Eger P., Zimmermann W., Wambutt R., Purnelle B.,	;	;	;	;
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelauré V., Mottier S.,	;	;	;	;
RA Gilabert F., Aves F.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,	;	;	;	;
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,	;	;	;	;
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Ray P., Benito J.,	;	;	;	;
RA Dominguez A., Reyna J.L., Moreno J., Armstrong J., Forsburg S.L.,	;	;	;	;
RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,	;	;	;	;
RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,	;	;	;	;
RT "The genome sequence of Schizosaccharomyces pombe.";	;	;	;	;
RL Nature 415:871-880 (2002).	;	;	;	;
CC -I- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.	;	;	;	;
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.	;	;	;	;
CC -I- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY	;	;	;	;
CC (EI-E2 ATPASES). SUBFAMILY IV.	;	;	;	;
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CC DR EMBL: Z69731; CAA93618.1;	;	;	;	;
CC DR InterPro: IPR001757; ATPase_E1-E2.	;	;	;	;
CC DR InterPro: IPR001454; Hignase/hydrolase.	;	;	;	;
CC DR Pfam: PF0070; Hydrolase; 1.	;	;	;	;
CC DR PROSITE: PS00154; ATPase_E1_E2; 1.	;	;	;	;
CC KW Hypothetical protein; Hydrolase; Transmembrane; Phosphorylation;	;	;	;	;
CC FT TRANSMEM	133	POTENTIAL.	;	;
CC FT TRANSMEM	153	;	;	;
CC FT TRANSMEM	274	294	POTENTIAL.	;
CC FT TRANSMEM	344	364	POTENTIAL.	;
CC FT TRANSMEM	344	373	POTENTIAL.	;
CC FT TRANSMEM	768	788	POTENTIAL.	;
CC FT TRANSMEM	843	863	POTENTIAL.	;
CC FT TRANSMEM	913	933	POTENTIAL.	;
CC FT TRANSMEM	939	959	POTENTIAL.	;
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CC DR EMBL: Z69731; CAA93618.1;	;	;	;	;
CC DR InterPro: IPR001757; ATPase_E1-E2.	;	;	;	;
CC DR InterPro: IPR001454; Hignase/hydrolase.	;	;	;	;
CC DR Pfam: PF0070; Hydrolase; 1.	;	;	;	;
CC DR PROSITE: PS00154; ATPase_E1_E2; 1.	;	;	;	;
CC KW Hypothetical protein; Hydrolase; Transmembrane; Phosphorylation;	;	;	;	;
CC FT TRANSMEM	133	POTENTIAL.	;	;
CC FT TRANSMEM	153	;	;	;
CC FT TRANSMEM	274	294	POTENTIAL.	;
CC FT TRANSMEM	344	364	POTENTIAL.	;
CC FT TRANSMEM	344	373	POTENTIAL.	;
CC FT TRANSMEM	768	788	POTENTIAL.	;
CC FT TRANSMEM	843	863	POTENTIAL.	;
CC FT TRANSMEM	913	933	POTENTIAL.	;
CC FT TRANSMEM	939	959	POTENTIAL.	;

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CC EMBL; L27081; AAH41577.1; -.

CC PIR; JC2193; JC2193; -.

CC InterPro; IPR000276; GPCR_Rhodopsin.

CC PFam; PF00001; 7cm_1; 1.

CC PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.

CC PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Lipoprotein; Palmitate.

DR DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 38 61 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 62 73 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 74 97 2 (POTENTIAL).

FT DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 115 138 3 (POTENTIAL).

FT DOMAIN 139 155 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 156 179 4 (POTENTIAL).

FT DOMAIN 180 186 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 187 211 5 (POTENTIAL).

FT DOMAIN 212 239 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 240 265 6 (POTENTIAL).

FT DOMAIN 266 273 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 274 297 7 (POTENTIAL).

FT DOMAIN 298 325 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 2 2 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 15 15 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 28 28 N-LINKED (GLCNAC . .) (POTENTIAL).

FT LIPID 311 311 PALMITATE (POTENTIAL).

FT LIPID 312 312 PALMITATE (POTENTIAL).

SQ SEQUENCE 325 AA; 37050 MW; 4E19FF1ABEA6BDC CRC64;

Query Match 4.2%; Score 97.5; DB 1; Length 325;

Best Local Similarity 19.2%; Pred. No. 2.9; Gaps 17;

Matches 64; Conservative 67; Mismatches 114; Indels 89;

Db 41 EVFLIGLVLSSL--ENILV--IGAVTKRNKLH-----SPMFVFGSLAVADMIVSM 87

Qy 185 ----TYOLYY---SLISAEVPLGRVVLMLVPSLVSYTGYATLICNMIAIQI-KYDD--YK 232

Db 88 SNAWETTIVYLINNKRHVIADTFVRHNDVFDMSICSVASMCSSLIAAVDRYITFYA 147

Qy 233 IRLGPL-----EVLCITIWRITLEITSRLILVLVSA---TLKLRAVFLVLFILIFE 283

Db 148 LRYHHMATTARSGVVIACIW-TFCISCGIVPIIYESKYYVIVCLISMFTMLFMYSLYI 206

Qy 284 PWIKFWRSG---AOMP--NNIEKNSRVRGTLVVLVISITLYAGINFSCWSALQLRLADR 337

Db 207 HMFLLARNHVRKIAASPRYNSTRQRASMKGA---ITLTM-LGIFIVCWSPEFLHII-- 259

Qy 338 DLVDKGQNWGHNGLHYSVRLVENIVMLVPKFFGKVLYNCHSLLALQLIAYLISIDF 397

Db 260 -----LMISCPQNYCACFMSTFNMVLLIMCNVID----- 291

Qy 398 MLLFFQYLHPIRSLSFTNVVDYLHCVVCHQHPRP 431

Db 292 ----PLIVALRSQEMRRT--PKEIICCHGFRRT 318